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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 05:36:47 ; Search time 87 Seconds
(without alignments)
774.819 Million cell updates/sec

Title: US-09-895-298A-83
Perfect score: 1002
Sequence: 1 MMNFQPPSKAMRASQMTFF.....HDGSLDLRSRSVQEGNPRA 190

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published.Applications.NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09895298 -ECGN_1_1_36_ernat_06112002_160417_2436
-NCPU=6 -ICPU=3 -NO_XIPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published.Applications.NA:*

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	177	17.7	454	10	US-09-864-761-11449 Sequence 11449, A
2	148	14.8	94	10	US-09-864-761-28040 Sequence 28040, A
3	107.5	10.7	2543	12	US-10-044-090-654 Sequence 654, App
4	93.5	9.3	1442	10	US-09-070-927A-680 Sequence 680, App

5	91	9.1	485	10	US-09-747-155-315	Sequence 315, App
6	91	9.1	487	10	US-09-747-155-325	Sequence 325, App
7	89	8.9	487	10	US-09-747-155-328	Sequence 328, App
8	86	8.6	969	10	US-09-866-055-254	Sequence 254, App
9	85.5	8.5	408	10	US-09-867-701-4424	Sequence 4424, App
10	84.5	8.4	32768	10	US-09-070-927A-100	Sequence 100, App
11	84	8.4	607	10	US-09-770-149-903	Sequence 903, App
12	82	8.2	458	10	US-09-747-155-216	Sequence 216, App
13	82	8.2	487	10	US-09-747-155-222	Sequence 222, App
14	82	8.2	1800	10	US-09-070-927A-786	Sequence 786, App
15	82	8.2	32200	10	US-09-764-847-1804	Sequence 1804, App
16	81.5	8.1	1515	10	US-09-833-381-1904	Sequence 1904, App
17	81.5	8.1	1515	10	US-09-833-381-1905	Sequence 1905, App
18	81	8.1	913	10	US-09-822-830A-168	Sequence 168, App
19	81	8.1	6651	10	US-09-954-456-1178	Sequence 178, App
20	81	8.1	6651	10	US-09-954-456-1217	Sequence 1217, App
21	80.5	8.0	1168	10	US-09-778-844-43	Sequence 43, App
22	80	8.0	486	10	US-09-747-155-191	Sequence 191, App
23	80	8.0	487	10	US-09-747-155-199	Sequence 199, App
24	80	8.0	487	10	US-09-747-155-208	Sequence 208, App
25	79.5	7.9	1051	10	US-09-809-545A-60	Sequence 60, App
26	79	7.9	924	10	US-09-825-882-17	Sequence 17, App
27	78.5	7.8	1812	10	US-09-750-240-3	Sequence 3, App
28	78.5	7.8	3549	10	US-09-750-240-5	Sequence 5, App
29	78	7.8	486	10	US-09-747-155-205	Sequence 205, App
30	78	7.8	7258	10	US-09-790-988-3	Sequence 3, App
31	77.5	7.7	1788	10	US-09-815-242-4189	Sequence 4189, App
32	77.5	7.7	1815	10	US-09-815-242-8427	Sequence 8427, App
33	77.5	7.7	23822	10	US-09-964-824A-572	Sequence 572, App
34	77.5	7.7	84539	10	US-09-962-436-36	Sequence 36, App
35	77	7.7	833	12	US-10-001-879-29	Sequence 29, App
36	77	7.7	1815	10	US-09-841-132-539	Sequence 539, App
37	76.5	7.6	45845	10	US-09-927-091-6	Sequence 6, App
38	76	7.6	382	10	US-09-864-761-18982	Sequence 18982, App
39	76	7.6	1731	10	US-09-764-869-1753	Sequence 1753, App
40	76	7.6	1731	10	US-09-764-869-1754	Sequence 1754, App
41	76	7.6	3552	10	US-09-750-240-10	Sequence 10, App
42	76	7.6	3582	10	US-09-750-240-12	Sequence 12, App
43	76	7.6	12017	10	US-09-735-927-3	Sequence 3, App
44	76	7.6	465237	10	US-09-933-267A-1	Sequence 1, App
45	75.5	7.5	848	10	US-09-908-808B-35	Sequence 35, App

ALIGNMENTS

RESULT 1
US-09-864-761-11449
Sequence 11449, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30

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/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 11449
/ LENGTH: 454
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC003108.1
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.69
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.74
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.67
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.75
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.62
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.78
US-09-864-761-11449

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Score: 177.00 Matches: 62
Percent Similarity: 48.63% Conservative: 9
Best Local Similarity: 42.47% Mismatches: 34
Query Match: 17.66% Indels: 41
DB: 10 Gaps: 8

US-09-895-298A-83 (1-190) x US-09-864-761-11449 (1-454)
QY 37 AlaIleThrIleTrpArgIleuLysProSerAla-----AspCysGlyPProphearg 53
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Db 15 GCAGCCGACTTCTGGAGGCTTCTCTCAAGCCTGTAGGGGAATTGC-----TTTAGA 68
QY 54 GlyLeuProLeuPheIleHisSerIleTyrSerTrpIleAspThrLeuSerThrArgPro 73
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 69 GGA-----GAAATTACAGT-----GCA 86
QY 74 GlyTyrLeuTrp---ValValTrpIleTyrArgAsnLeuIleGlySerValHisPhephe 92
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Db 87 GGAAGGCTCTGGGGGATTAATCGGTTTACTGTGAATGTTT-----CTTTTC 134
QY 93 PheIleLeuThrIleuIleValLeuIleIleThrTyrLeuTyrTrpGlnIleThrGluGly 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 TTTCACCAAAAGATGGCAGTAACTTCATCCACTTCTAGGATCCTAGCTGCCTGAAC 194
QY 113 ArgLysIleMetIleArgLeuLeu-----HisGluGlnIle-Ileasn----- 126
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Db 195 CGACGTTCTTCCATCAATGCTTCTCATTCATCCATCATCATCATCATTTTGT 254
QY 127 -----GluGlyLysAspLysMetPheLeuIleG1 136
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Db 255 TTCTTTCTGTTTGTCTTCTCTTCTGTAGAGAGGCAAAAGATAAATGTTCTGTAGA 314
QY 136 uLysLeuIleLysLeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuG1 156
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Db 315 AAATTCATCAAGCTGCAGATATGAGAGAAGCAACCCAGCTCACTGTCTGGA 374
QY 156 uArgArgGluValGlu 161
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Db 375 AAGAGAGAGCTGGAG 390

RESULT 2
US-09-864-761-28040
/ Sequence 28040, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharron G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
/ FILE REFERENCE: Aecomica-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
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/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 28040
/ LENGTH: 94
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC003108.1
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.69
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.74
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.67
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.75
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.62
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.78
/ OTHER INFORMATION: NT HIT: AJ276505.1, EVALUE 5.00e-02
/ OTHER INFORMATION: EST_HUMAN HIT: AW582253.1, EVALUE 5.00e-46
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US-09-864-761-28040

Alignment Scores:

Pred. No.:	1.36e-10	Length:	94
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DB:	10	Gaps:	0

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QY 151 SerSerleuValleuGluArgArgGluValGlu 161

Db 62 AGTCACCTGTCTCTGGAAGAGAGAGGTGAG 94

RESULT 3

US-10-044-090-654

; Sequence 654, Application US/10044090

; Patent No. US20020137081A1

; GENERAL INFORMATION:

; APPLICANT: Olga Bandman

; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION

; FILE REFERENCE: PA-0028 US

; CURRENT APPLICATION NUMBER: US/10/044,090

; CURRENT FILING DATE: 2002-01-09

; NUMBER OF SEQ ID NOS: 850

; SOFTWARE: PERL Program

; SEQ ID NO 654

; LENGTH: 2543

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID NO. US20020137081A1 1450758CBI

US-10-044-090-654

Alignment Scores:

Pred. No.:	0.00218	Length:	2543
Score:	107.50	Matches:	47
Percent Similarity:	37.31%	Conservative:	28
Best Local Similarity:	23.38%	Mismatches:	55
Query Match:	10.73%	Indels:	71
DB:	12	Gaps:	10

US-09-895-298a-83 (1-190) x US-10-044-090-654 (1-2543)

QY 6 ProProSerLysAlaTrpArgAla-----SerGlnMetMetThrPhePhe 20

Db 123 CCTCTGGTCGAGCCTGGCGCGCCGACCATGGCCATCGCTCAACTGGCCACGGAGTAC 182

QY 21 IlePheLeuLeuPhePhe-----ProSerPheThrGlyValLeuGly 34

Db 183 GTGTTCTCGAATTCTTCTGTAAGAGAGCCGAGCCCAAGTCAAGGGGCTGCGACTG 242

QY 35 ThrLeuAlaIleThrIleTrpArgLeuLysProSerAlaAspCysGlyProPheArgGly 54

Db 243 GAGCTGGCTGTG-----GACAAAGATGTTACGTCATTGGGGTG---GGG 284

QY 55 LeuProLeuPheIleHisSerIle-----GACAAAGATGTTACGTCATTGGGGTG---GGG 284

Db 285 CTGCCCTGCTGCTCATCTGCTGGCTTGGCGAGAGATCTCGATTGGTACACAGATA 344

QY 63 -----TyrSerTrp-----IleAspThrLeuSer 70

Db 345 AGCTGTTTCTCTCCAAAGTCTTCTCTGCGTACAGGCTGCTTGTGATGATCA----- 398

QY 71 ThrArgProGlyTyrLeuTrpValValTrpIleTyrArgAsnLeuIleGlySer----- 88

Db 399 -----TATGCTGGCGGCTGTTCAGCAGAGAACTCATCTGACAGGAGTCT 446

QY 89 -----ValHisPhePhePhe-----IleLeuThrLeuIle 98

Db 447 GGAACCTCCCACTGTGGCTGCATTAAGTTTTCCTTACATCTGCTGCTTTGCGATC 506

QY 99 ValLeuIleIleThrTyrLeuTyrTrpGlnIleThrGluGlyArgLysIleMetIleArg 118

Db 507 CTCTGTACCTGCCCGCGCTGTTCGGCGTTTCGACGCTGCTCATATTGTC----- 560

QY 119 LeuLeuHisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeu 138

Db 561 -----TCAGACTGAAGTTTATCATGAGAACTT 590

QY 139 IleLysLeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValleuGluArg 158

Db 591 GACAAAGTTTACAAACCGTGCAATTAAAGCTGCAAGAGTGGCGGTGACCTTGACATGAGA 650

QY 159 Glu 159

Db 651 GAT 653

RESULT 4

US-09-070-927A-680

; Sequence 680, Application US/09070927A

; Patent No. US20020120116A1

; GENERAL INFORMATION:

; APPLICANT: Charles A. Kunsch

; APPLICANT: Patrick J. Dillon

; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides

; NUMBER OF SEQUENCES: 982

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/070,927A

; FILING DATE: 04-May-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/046,655

; FILING DATE: 1997-05-16

; APPLICATION NUMBER: 60/044,031

; FILING DATE: 1997-05-06

; APPLICATION NUMBER: 60/066,009

; FILING DATE: 1997-11-14

; ATTORNEY/AGENT INFORMATION:

; NAME: Kenley K. Hoover

; REGISTRATION NUMBER: 40,302

; REFERENCE/DOCKET NUMBER: PB369

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8512

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 680:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1442 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 680:

US-09-070-927A-680

Alignment Scores: 0.0494 Length: 1442

Score: 93.50 Matches: 42
Percent Similarity: 42.25% Conservative: 18
Best Local Similarity: 29.58% Mismatches: 57
Query Match: 9.33% Indels: 25
DB: 10 Gaps: 7

US-09-895-298a-83 (1-190) x US-09-070-927a-680 (1-1442)

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QY 44 LysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheLeuHisSerIleTyr 63
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Db 1003 AAAATGAGTGCATTTTATAGGCTCATCATCTTTATAGCATTTATCGTAACCTCTGTATAT 1062
QY 64 SerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrpIleTyrArg 83
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Db 1063 TTGTCTTACTGTATTTTAAAGAGAGAAATAATTATCCCTATTTGTATGATTTATATG 1122
QY 84 AsnLeuIleGlySerValHisPhePheLeuThrLeuIleVal-----Leu 100
    ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1123 ATTCTATTTGATTA-----TTTTCMCTGCGTTAGAGTTATTTATCCAGTACATAT 1176
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlyArgLysIleMetIleArgLeu 120
    ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1177 TTCTCTTACTATTTTCATTTGATTAATAATATTAAAGAKCCAAAACAAAG---GAATTGCTA 1233
QY 121 HisGluGlnIleLeuAsnGlyLysAspLysMetPheLeuIleGlyLysLeuIleLys 140
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1234 CATGACGAAGAATAAAGCAACMGAAAA-----ATAATGAAAAAACAAACCCCT 1284
QY 141 LeuGlnAspMet---GluLysLysAlaAsnProSerSerLeuValLeuGluArgGlu 159
    ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1285 ATTCAGAAATTCACAGAAAGTAATTCAAAAGCAAAAAGATCTA-----AATCAGAAA 1335
QY 160 Val-----GluGlnGlnGlyPheLeuHis 167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1336 GTTGCTTCACATATTCTAACGATTATATCCCTCGATTAATAAAGCTGGCTATTCAT 1395
QY 168 LeuGly 169
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Db 1396 CTTGGC 1401
```

RESULT 5
US-09-747-155-315

```
; Sequence 315, Application US/09747155
; Patent No. US20020151692A1
; GENERAL INFORMATION:
; APPLICANT: Rouquier, Sylvie
; TITLE OF INVENTION: No. US20020151692A1el Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 19904-008 (C009B6834US)
; CURRENT APPLICATION NUMBER: US/09/747,155
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,746
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 431
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 315
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Pongo pygmaeus
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(486)
; OTHER INFORMATION: Taxon = 9600; gene = PPY112; Accession DDBJ/EMBL/GenBank = AF1798
; NAME/KEY: CDS
; LOCATION: (1)..(486)
; OTHER INFORMATION: Product = olfactory receptor
US-09-747-155-315
```

Alignment Scores:

Pred. No.: 0.019 Length: 486
Score: 91.00 Matches: 37
Percent Similarity: 44.72% Conservative: 18
Best Local Similarity: 30.08% Mismatches: 45

Query Match: 9.08% Indels: 23
DB: 10 Gaps: 7
US-09-895-298a-83 (1-190) x US-09-747-155-315 (1-486)

```
QY 6 ProProSer-----LysAlaTrp-----ArgAlaSerGln 15
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 29 CCACCATCATGAGTCAGAGCCAGTGTGTCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 88
QY 16 MetMetThrPhePheIlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThr 35
    ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 GTGCGTGCTCTTTTGCAATACCCCTCTCTGCGCCGCTTCTCTGCTGCTGCTGCTGCTGCTGCT 148
QY 36 LeuAlaIleThr---IleTrpArgLeuLysProSerAlaAspCysGlyPro-PheArgGlu 54
    ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 TCATCTCTCCTCTCTCTCTCTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 205
QY 54 yLeuProLeuPheIleHisSerIleTyrSerTrpIleAsp-----ThrLeuSer 70
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 206 CCTCCCTCATCATGAGTTAGCAATCTTTACAGCAGGATTACAGCCATTATGCTTCCATTCC 265
QY 70 rThrArgProGlyTyrLeuTrpValValTrpIleTyrArgAsnLeuIleGlySerValHis 90
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 266 TGTGCATTCCTGTTCTTCTATGTCACATTTGGGCTCAC---CATCTCCAGATTCCTCCCA 322
QY 90 sPhePhePheIleLeuThrLeuIleValLeuIleIle-----ThrTyrLe 105
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 CCAAGGCATATGCAAGCCTTGTCACACTTGTCGATCCACCTCTCAGTGTGACTATCT 382
QY 105 uTyrTrp 107
    |||
Db 383 ATTATGG 389
```

RESULT 6
US-09-747-155-325

```
; Sequence 325, Application US/09747155
; Patent No. US20020151692A1
; GENERAL INFORMATION:
; APPLICANT: Rouquier, Sylvie
; TITLE OF INVENTION: No. US20020151692A1el Polypeptides and Nucleic Acids Encoding
; FILE REFERENCE: 19904-008 (C009B6834US)
; CURRENT APPLICATION NUMBER: US/09/747,155
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,746
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 431
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 325
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Pongo pygmaeus
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(487)
; OTHER INFORMATION: Taxon = 9600; gene = PPY118; Accession DDBJ/EMBL/GenBank = AF1
; NAME/KEY: CDS
; LOCATION: (2)..(487)
; OTHER INFORMATION: Product = olfactory receptor
US-09-747-155-325
```

Alignment Scores:

Pred. No.: 0.0191 Length: 487
Score: 91.00 Matches: 37
Percent Similarity: 44.72% Conservative: 18
Best Local Similarity: 30.08% Mismatches: 45
Query Match: 9.08% Indels: 23
DB: 10 Gaps: 7

US-09-895-298a-83 (1-190) x US-09-747-155-325 (1-487)

```
QY 6 ProProSer-----LysAlaTrp-----ArgAlaSerGln 15
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

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Db 30 CCACCATCATGAGTACAGAGCCAGTGTGATGCTGGTGGCTGCTCGGTCATCGCTT 89
Qy 16 MetMetThrPhePheIlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThr 35
Db 90 GTGGCTGTGCTCTTTTGGCATACCTCCTCTGTGGCCGGCTTCTCTGTGTGTGACACACA 149
Qy 36 LeuAlaIleThr---IleTrpArgLeuLysProSerAlaAspCysGlyPro-PheArgG1 54
Db 150 TCATCTCTCACTTCTTCTGTGACCTTGGTGGCCCTGCTCAAGCTGT---CCTGCTCAGACA 206
Qy 54 YLeuProLeuPheIleHisSerIleTyrSerTrpIleAsp-----ThrLeuSe 70
Db 207 CCTCCCTCAATCATGATTAGCAATCTTACACAGAGATTGACAGCCATTATGCTTCATTCC 266
Qy 70 rThrArgProGlyTyrIleuTrpValValTrpIleTyrArgAsnLeuIleGlySerValHi 90
Db 267 TGTGATCTCTGTCTTCTTATGTGTACATTGGGGGTAC---CATCTCCAGATTCCCTCCA 323
Qy 90 sPhePhePheIleLeuThrLeuIleValLeuIleIle-----ThrTyrIle 105
Db 324 CCAAGGGCATATGCAAAAGCCTTGTCCACCTGTGATCCACCTCTCACTGATGCTGACTATCT 383
Qy 105 uTyrTrp 107
Db 384 ATTAGG 390

RESULT 7
US-09-747-155-328
; Sequence 328, Application US/09747155
; Patent No. US20020151692A1
; GENERAL INFORMATION:
; APPLICANT: Rouquier, Sylvie
; APPLICANT: Giorzi, Dominique
; TITLE OF INVENTION: No. US20020151692A1 Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 19904-008 (C009B6834US)
; CURRENT APPLICATION NUMBER: US/09/747,155
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,746
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 431
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 328
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Pongo pygmaeus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(487)
; OTHER INFORMATION: Taxon = 9600; gene = PPY120; Accession DDBJ/EMBL/GenBank = AF1798
; NAME/KEY: CDS
; LOCATION: (2)..(487)
; OTHER INFORMATION: Product = olfactory receptor
US-09-747-155-328

Alignment Scores:
Pred. No.: 0.0338 Length: 487
Score: 89.00 Matches: 33
Percent Similarity: 48.11% Conservative: 18
Best Local Similarity: 31.13% Mismatches: 42
Query Match: 8.88% Indels: 13
Gaps: 10

US-09-895-298A-83 (1-190) x US-09-747-155-328 (1-487)
Qy 13 AlaSerGlnMetMetThrPhePheIlePheLeuLeuPhePheProSerPheThrGlyVal 32
Db 81 TCATCGCTGTGGGTGTGCTCTTTGGCATACCTCCTTCTGGCCGGCTTCTCTGTG 140
Qy 33 LeuGysThrLeuAlaIleThr---IleTrpArgLeuLysProSerAlaAspCysGlyPro 51
Db 141 CTGACCACATCATCCCTCACTTCTGTGACACTTGTGACCTTGTGACCTCAAGCTGT---CCT 197
Qy 52 -PheArgGlyLeuProLeuPheIleHisSerIleTyrSerTrpIleAsp----- 67
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Db 198 GCTCAGACACCTCCCTCATATCAGTTAGCAATCTTTACAGCAGAGATTGACACCATATATGC 257
Qy 68 -ThrLeuSerThrArgProGlyTyrLeuTrpValValTrpIleTyrArgAsnLeuIleG1 87
Db 258 TTCCATTCTCGTGCATCCTGTGTTCTTATGTGCACATTTGGGGTCAAC---CATCCATCACA 314
Qy 87 ySerValHisPhePhePheIleLeuThrLeuIleValLeuIleIle----- 102
Db 315 TTCCCTCCACCAAGGCATATGCAAAAGCCTGTGCACCTGTGTGATGCCACCTCTCAGTGG 374
Qy 103 -ThrTyrLeuTyrTrp 107
Db 375 TGACTATCTATATAGG 390

RESULT 8
US-09-886-055-254
; Sequence 254, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 254
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-886-055-254

Alignment Scores:
Pred. No.: 0.228 Length: 969
Score: 86.00 Matches: 35
Percent Similarity: 42.86% Conservative: 22
Best Local Similarity: 26.32% Mismatches: 51
Query Match: 8.58% Indels: 25
Gaps: 10

US-09-895-298A-83 (1-190) x US-09-886-055-254 (1-969)
Qy 1 MetMetAsnPheGlnProProSer-----LysAlaArgP----- 11
Db 383 ATCTCTACATATATGCCACCATCATGACTCAGAGCCAGTGTGCATGCTGGTGGCTGGGT 442
Qy 12 --ArgAlaSerGlnMetMetThrPhePheIlePheLeuLeuPhePheProSerPheThr 30
Db 443 CCTGGGTCATCGCTTGTGGCTGTGCTCTTTGCATACCTCCTCTGGCCAGCTTTCCT 502
Qy 31 GlyValLeuCysThrLeuAlaIleThrIle---TrpArgLeuLysProSerAlaAspCys 49
Db 503 TCTGTGTGACACATCATCCCTCACTACTTGTGTGACCTTGTGACCTTGTGACCTCAAGTGT 562
Qy 50 GlyPro-PheArgGlyLeuProLeuPheIleHisSerIleTyrSerTrpIleAsp----- 67
Db 563 ---CCTGCTCAGACACCTCCCTCAATCATGTTAGCAATCTTTACAGCAGCATTTGACAGCCA 619
Qy 68 -----ThrLeuSerThrArgProGlyTyrLeuTrpValValTrp----- 80
Db 620 TTATGCTTCATCTCTGTGCATCCTGCTTCTTATGTGCACATTTGGGGTCAACATCCTCC 679
Qy 81 -----IleTyrArgAsnLeuIleGlySer---ValHisPhePhePheIleLeuThrIle 97
Db 680 AGATTCCCTCTACCAAGGCATATGCAAAAGCCTTGTGCACCTTGTGATGCCACCTCTCAG 739
Qy 97 uIleValLeuIleIleThrTyrLeuTyrTrpGlnIle 109
```



```
; Sequence 903, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 903
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(607)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-149-903

Alignment Scores:
Pred. No.: 0.197 Length: 607
Score: 84.00 Matches: 28
Percent Similarity: 43.97% Conservative: 23
Best Local Similarity: 24.14% Mismatches: 44
Query Match: 8.38% Indels: 21
DB: 10 Gaps: 5

US-09-895-298a-83 (1-190) x US-09-770-149-903 (1-607)
QY 16 MetMetThrPhePheIlePheLeuLeuPheProSerPheThrGlyValLeuCysThr 35
DB 76 ATACTCAATTCTCTAGTATTCTNNCTCGATCCCAATCTTAGCTGT----- 123
QY 36 LeuAlaIleThrIleTrp--ArgLeuLysProSerAlaAspCysGlyProPheArgGly 54
DB 124 -----GGAAATCTGGCTAAGCCAAAGGTCACAGAGTGAAGATTCCTAGAC 174
QY 55 LeuProLeuPheIleHisSerIleTyrSerTrpIleAspThrLeuSerThrArgProGly 74
DB 175 AAACCAAGTAGATTGCTCTTGGTGTTCCTTATGTTGAGCATAGCTGGTCTAATAGGT 234
QY 75 -----TyrLeuTrpValValTrpIleTyrArgAsnLeuIleGlySerValHis 90
DB 235 TCATGTTGTAGAGTCACATGGCTTCTTGGGTTAT-----CTCTTT 276
QY 91 PhePhePheIleLeuThrIleValLeuIleIleThrTyrLeuTyrTrpGlnIleThr 110
DB 277 GTCATGTTCTTTGATTCTCTGTTGTTCTGTATACAGATTTTGGCTTTGTTGTTACT 336
QY 111 GluGlyArg-LysIleMetIleArgLeuLeuHisGluGlnIleIle 125
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DB 337 -----AACAAAGAGCTGTGTGAAGCTATTGAAGGAAAAGGTTATA 376
RESULT 12
US-09-747-155-216
; Sequence 216, Application US/09747155
; Patent No. US20020151692A1
; GENERAL INFORMATION:
; APPLICANT: Rouquier, Sylvie
; APPLICANT: Giorgi, Dominique
; TITLE OF INVENTION: NO. US20020151692A1el Polypeptides and Nucleic Acids Encoding
; FILE REFERENCE: 19904-008 (C009B6834US)
; CURRENT APPLICATION NUMBER: US/09/747,155
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,746
; NUMBER OF SEQ ID NOS: 431
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 216
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Gorilla gorilla
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(458)
; OTHER INFORMATION: Taxon = 9593; gene = GG0104; pseudogene; Accession DDBJ/EMBL/
US-09-747-155-216

Alignment Scores:
Pred. No.: 0.226 Length: 458
Score: 82.00 Matches: 37
Percent Similarity: 42.06% Conservative: 16
Best Local Similarity: 29.37% Mismatches: 44
Query Match: 8.18% Indels: 29
DB: 10 Gaps: 8

US-09-895-298a-83 (1-190) x US-09-747-155-216 (1-458)
QY 6 ProProSer-----LysAlaTrp-----ArgAlaSerGln 15
DB 1 CCACCATCATGAGTCACAGCCAGTGTGCATGCTGGTGGCTGGCTGGTATCGCTT 60
QY 16 MetMetThrPhePheIlePheLeuLeuPheProSerPheThrGlyValLeuCysThr 35
DB 61 GTGGGTGTCTCTTTGCATACCTCTCTGCGCCGGCTTCTCTGTGTGACACACA 120
QY 36 LeuAlaIleThr--IleTrpArgLeuLysProSerAlaAspCysGlyPro-PheArgI 54
DB 121 TCATCCCTCACTTCTCTGTGACCTTGTGCGCCCTGCTCAAGTTGT---CCTGCTCAGACA 177
QY 54 yLeuProLeuPheIleHisSerIleTyrSerTrpIleAsp-----ThrLeuSe 70
DB 178 CTTCCCTCAATCAGTTAAGCAATCTTTACAGCAGATGACAGCCATTATGCTTCCATTGCC 237
QY 70 rThrArgProGlyTyrLeuTrpValValTrp-----IleTyrArg 83
DB 238 TGTGCATCTGTGTTCTTATGTCACATGTGGGGTCAACATCCTCCAGATTCCCTACCA 297
QY 83 gAsnLeuIleGlySer---ValHisPhePhePheIleLeuThrLeuIleValLeuIleI 102
DB 298 AGGCATATGCAAGACCTTGTCCAC-----TTGTGATCCACACCTTCAGTGG 345
QY 102 eThrTyrLeuTyrTrp 107
DB 346 TGACTATCTATATATGG 361

RESULT 13
US-09-747-155-222
; Sequence 222, Application US/09747155
; Patent No. US20020151692A1
; GENERAL INFORMATION:
; APPLICANT: Rouquier, Sylvie
; APPLICANT: Giorgi, Dominique
; TITLE OF INVENTION: NO. US20020151692A1el Polypeptides and Nucleic Acids Encoding
```



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Db      1707 GCATCACC GTGGCCAAAGAATAGTTGCAATTA 1742
          |||      ::||| |||

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RESULT 15

US-09-764-847-1804/C

; Sequence 1804, Application US/09764847

Patent No. US20020132767A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

1. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC009

; CURRENT APPLICATION NUMBER: US/09/764,847
 ; CURRENT FILING DATE: 2001-01-17

```

; CURRENT FILING DATE: 2001-01-17
; Prior application data removed

```

NUMBER OF SEQ ID NOS: 2003

NUMBER OF SEQ ID NOS: 2003
SOFTWARE: PatentIn Ver 2.0

; SOFTWARE: PatentIn ver. 2.0
: SEO ID NO 1804

```

; SEQ ID NO 1604
: LENGTH: 3220

```

LENGTH: 32200
TYPE: DNA

ORGANISM:

ORGANISM: HOMO SAPIENS
US-09-764-847-1804

C
C
C
C
C
C
C
T
C
C

Alignment Scores:

Pred. No.:	153	Length:	32200
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Score: 82.00

Percent Similarity:	42.28%	Conservative:	29%
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Best Local Similarity:	22.82%	Mismatches:	47
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Query Match:	8.18%	Indels:	39
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DB:	10	Gaps:	6
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US-09-895-298A-83 (1-190) x US-09-764-847-1804 (1-32200)

36 LeuAlaIleThrIleTparGleuLysProSerAlaaspCysGlyProPheargGlyLeu 55

Db 2602 ATGATAATCTCTACATTCTCTCCTGAAGCCTCTGACTGTCAAGCATCAGA---AGA 2546

56 ProLeuPheIleHisSerIleTyrSerTrpIleAspThrLeuSerThrArgProGly--- 74

Db 2545 GATCTCTTCAACA---AGTCTCAGAAAGTGGCTGATGATGTCACGTCTAGGCTTGCACA 2489

QY 75 ---TyrLeuTrpValTrrIleTyrArgAsnLeuIle-GlySerValHisPhePhe 93

Db 2488 GTATTCTCTTCTAGTGGGGAAGAGAGAAACATTAAATTAAATTACATTCTATAT 2429

93 eileleuthrleuilevalleuileilethrtyrleutyrr----- 106

Db 2428 ATCATACAATTATCTAGTTAGCCATACATATTAGTTCTTCTCACACTCCTATGAAG 2369

QY 107 -----TrpGlnIleThrGluGly----- 112

Db 2368 AAATACCCAAGACTGGTATTATTAAAGGAAGAGTTTAACTGACTACAGTTCTGCA 2308

```

0v 113 -----Arctivst]eMett]eArv-----fc 118

```

[illegible]

Q. 116 How many of the 1000 people who were interviewed in the survey were aged 18 or over?

[illegible]

0
4
3
5
4
4
3
2
2
1
1
2
2
1

[illegible]

Search completed: November 9, 2002, 07:26:21
Job time : 103 secs

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